

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Bartley, Timothy D.  
Bogenberger, Jakob M.  
Bosselman, Robert A.  
Hunt, Pamela  
Samal, Babru B.

(ii) TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR STIMULATING  
MEGAKARYOCYTE GROWTH AND DIFFERENTIATION

(iii) NUMBER OF SEQUENCES: 34

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Amgen Inc.  
(B) STREET: 1840 Dehavilland Drive  
(C) CITY: Thousand Oaks  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 91320-1789

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/347,780  
(B) FILING DATE: 30-NOV-1994  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/252,628  
(B) FILING DATE: 31-MAY-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/221,768  
(B) FILING DATE: 31-MAR-1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/321,488  
(B) FILING DATE: 12-OCT-1994

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Cook, Robert R.  
(B) REGISTRATION NUMBER: 31,602  
(C) REFERENCE/DOCKET NUMBER: A-290C

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids  
(B) TYPE: amino acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Ala	Pro	Pro	Ala	Xaa	Asp	Pro	Arg	Leu	Leu	Asn	Lys	Met	Leu	Arg	Asp
1				5					10					15	
Ser	His	Val	Leu	His	Xaa	Arg	Leu	Xaa	Gln	Xaa	Pro	Asp	Ile	Tyr	
		20						25					30		

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ala Pro Pro Ala Xaa Asp Pro Arg Leu Leu Asn Lys Met Leu Arg Asp  
1 5 10 15  
Ser His Val Leu His  
20

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Thr Gln Lys Glu Gln Thr Lys Ala Gln Asp Val Leu Gly Ala Val Ala  
1 5 10 15  
Leu

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCNCCNCCNG CNTGYGA

17

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

*C<sup>13</sup>*  
*wt.* (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GCARTGYAAC ACRTGNGART C

21

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg Asp  
1 5 10 15  
Ser His Val Leu His  
20

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GTACGCGTTC TAGANNNNN T

21

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AGTTTACTGA GGACTCGGAG G

21

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTCGGCCGGA TAGGCCTTTT TTTTTTTTTT

30

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

C<sup>13</sup>  
cont.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTCGGCCGGATAGGCCTTTT TTTTTTTTT

29

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGCGACCTCC GAGTCCTCAG

20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GAGTCCTCAG TAAACTGCTT CGT

23

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GGAGTCACGA AGCAGTTTAC

20

C<sup>13</sup>  
cont'

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCTTTACTTC TAGGCCTG

18

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

*C 13*  
*cont.* (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAGGTCACAA GCAGGAGGA

19

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGCATAGTCC GGGACGTCG

19

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TCCTCCTGCT TGTGACCTC

19

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCAGGAAGGA TTCAGGGGA

19

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CAACAAGTCG ACCGCCAGCC AGACACCCCG

30

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

C<sup>13</sup>  
cont.

GGCCGGATAG GCCACTCNNN NNNT

24

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCARTGYAAN ACRTGNGART C

21

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

*C13*  
*cont.*  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTGGTGTGCA CTTGTG

16

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

*(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:*

CACAAGTCCA CACCAACCCC

20

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1342 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 36..1097

(ix) FEATURE:

- (A) NAME/KEY: mat\_peptide
- (B) LOCATION: 99..1097

(ix) FEATURE:

- (A) NAME/KEY: sig\_peptide
- (B) LOCATION: 36..98

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CAGGGAGCCA CGCCAGCCAA GACACCCCGG CCAGA ATG GAG CTG ACT GAA TTG Met Glu Leu Thr Glu Leu -21 -20	53
CTC CTC GTG GTC ATG CTT CTC CTA ACT GCA AGG CTA ACG CTG TCC AGC Leu Leu Val Val Met Leu Leu Leu Thr Ala Arg Leu Thr Leu Ser Ser -15 -10 -5 1	101
CCG GCT CCT CCT GCT TGT GAC CTC CGA GTC CTC AGT AAA CTG CTT CGT Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg 5 10 15	149
GAC TCC CAT GTC CTT CAC AGC AGA CTG AGC CAG TGC CCA GAG GTT CAC Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val His 20 25 30	197
CCT TTG CCT ACA CCT GTC CTG CTG CCT GCT GTG GAC TTT AGC TTG GGA Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu Gly 35 40 45	245
GAA TGG AAA ACC CAG ATG GAG GAG ACC AAG GCA CAG GAC ATT CTG GGA Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly 50 55 60 65	293
GCA GTG ACC CTT CTG CTG GAG GGA GTG ATG GCA GCA CGG GGA CAA CTG Ala Val Thr Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu 70 75 80	341
GGA CCC ACT TGC CTC TCA TCC CTC CTG GGG CAG CTT TCT GGA CAG GTC Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val 85 90 95	389
CGT CTC CTC CTT GGG GCC CTG CAG AGC CTC CTT GGA ACC CAG CTT CCT Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro 100 105 110	437

B  
C  
cont.

CCA CAG GGC AGG ACC ACA GCT CAC AAG GAT CCC AAT GCC ATC TTC CTG Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu 115 120 125	485
AGC TTC CAA CAC CTG CTC CGA GGA AAG GTG CGT TTC CTG ATG CTT GTA Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu Met Leu Val 130 135 140 145	533
GGA GGG TCC ACC CTC TGC GTC AGG CGG GCC CCA CCC ACC ACA GCT GTC Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr Thr Ala Val 150 155 160	581
CCC AGC AGA ACC TCT CTA GTC CTC ACA CTG AAC GAG CTC CCA AAC AGG Pro Ser Arg Thr Ser Leu Val Leu Thr Leu Asn Glu Leu Pro Asn Arg 165 170 175	629
ACT TCT GGA TTG TTG GAG ACA AAC TTC ACT GCC TCA GCC AGA ACT ACT Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr Ala Ser Ala Arg Thr Thr 180 185 190	677
GGC TCT GGG CTT CTG AAG TGG CAG CAG GGA TTC AGA GCC AAG ATT CCT Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly Phe Arg Ala Lys Ile Pro 195 200 205	725
GGT CTG CTG AAC CAA ACC TCC AGG TCC CTG GAC CAA ATC CCC GGA TAC Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu Asp Gln Ile Pro Gly Tyr 210 215 220 225	773
CTG AAC AGG ATA CAC GAA CTC TTG AAT GGA ACT CGT GGA CTC TTT CCT Leu Asn Arg Ile His Glu Leu Leu Asn Gly Thr Arg Gly Leu Phe Pro 230 235 240	821
GGA CCC TCA CGC AGG ACC CTA GGA GCC CCG GAC ATT TCC TCA GGA ACA Gly Pro Ser Arg Arg Thr Leu Gly Ala Pro Asp Ile Ser Ser Gly Thr 245 250 255	869
TCA GAC ACA GGC TCC CTG CCA CCC AAC CTC CAG CCT GGA TAT TCT CCT Ser Asp Thr Gly Ser Leu Pro Pro Asn Leu Gln Pro Gly Tyr Ser Pro 260 265 270	917
TCC CCA ACC CAT CCT ACT GGA CAG TAT ACG CTC TTC CCT CTT CCA Ser Pro Thr His Pro Pro Thr Gly Gln Tyr Thr Leu Phe Pro Leu Pro 275 280 285	965
CCC ACC TTG CCC ACC CCT GTG GTC CAG CTC CAC CCC CTG CTT CCT GAC Pro Thr Leu Pro Thr Pro Val Val Gln Leu His Pro Leu Leu Pro Asp 290 295 300 305	1013
CCT TCT GCT CCA ACG CCC ACC CCT ACC AGC CCT CTT CTA AAC ACA TCC Pro Ser Ala Pro Thr Pro Thr Pro Thr Ser Pro Leu Leu Asn Thr Ser 310 315 320	1061
TAC ACC CAC TCC CAG AAT CTG TCT CAG GAA GGG TAA GGTTCTCAGA Tyr Thr His Ser Gln Asn Leu Ser Gln Glu Gly *	1107
325 330	
CACTGCCGAC ATCAGCATTG TCTCGTGTAC AGCTCCCTTC CCTGCAGGGC GCCCCTGGGA	1167

C<sup>13</sup>  
out

GACAACTGGA CAAGATTCC TACTTTCTCC TGAAACCAA AGCCCTGGTA AAAGGGATAC	1227
ACAGGACTGA AAAGGGAATC ATTTTCACT GTACATTATA AACCTTCAGA AGCTATTTT	1287
TTAAGCTATC AGCAATACTC ATCAGAGCAG CTAGCTCTT GGTCTATTTT CTGCA	1342

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 354 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

Met Glu Leu Thr Glu Leu Leu Val Val Met Leu Leu Leu Thr Ala  
-21 -20 -15 -10

Arg Leu Thr Leu Ser Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val  
-5 1 5 10

Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser  
15 20 25

Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala  
30 35 40

Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys  
45 50 55

Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met  
60 65 70 75

Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly  
80 85 90

Gln Leu Ser Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu  
95 100 105

Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp  
110 115 120

Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val  
125 130 135

Arg Phe Leu Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala  
140 145 150 155

Pro Pro Thr Thr Ala Val Pro Ser Arg Thr Ser Leu Val Leu Thr Leu  
160 165 170

Asn Glu Leu Pro Asn Arg Thr Ser Gly Leu Leu Glu Thr Asn Phe Thr  
175 180 185

C3  
cont.

Ala Ser Ala Arg Thr Thr Gly Ser Gly Leu Leu Lys Trp Gln Gln Gly  
190 195 200

Phe Arg Ala Lys Ile Pro Gly Leu Leu Asn Gln Thr Ser Arg Ser Leu  
205 210 215

Asp Gln Ile Pro Gly Tyr Leu Asn Arg Ile His Glu Leu Leu Asn Gly  
220 225 230 235

Thr Arg Gly Leu Phe Pro Gly Pro Ser Arg Arg Thr Leu Gly Ala Pro  
240 245 250

Asp Ile Ser Ser Gly Thr Ser Asp Thr Gly Ser Leu Pro Pro Asn Leu  
255 260 265

Gln Pro Gly Tyr Ser Pro Ser Pro Thr His Pro Pro Thr Gly Gln Tyr  
270 275 280

Thr Leu Phe Pro Leu Pro Pro Thr Leu Pro Thr Pro Val Val Gln Leu  
285 290 295

His Pro Leu Leu Pro Asp Pro Ser Ala Pro Thr Pro Thr Pro Thr Ser  
300 305 310 315

Pro Leu Leu Asn Thr Ser Tyr Thr His Ser Gln Asn Leu Ser Gln Glu  
320 325 330

Gly \*

C13  
cont.

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1164 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 97..891

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AGGGAGCCAC GCCAGCCAGA CACCCCGGCC AGAATGGAGC TGACTGAATT GCTCCTCGTG 60

GTCATGCTTC TCCTAACTGC AAGGCTAACG CTGTCC AGC CCG GCT CCT CCT GCT 114  
Ser Pro Ala Pro Pro Ala  
1 5

TGT GAC CTC CGA GTC CTC AGT AAA CTG CTT CGT GAC TCC CAT GTC CTT 162  
Cys Asp Leu Arg Val Leu Ser Lys Leu Leu Arg Asp Ser His Val Leu  
10 15 20

CAC AGC AGA CTG AGC CAG TGC CCA GAG GTT CAC CCT TTG CCT ACA CCT		210
His Ser Arg Leu Ser Gln Cys Pro Glu Val His Pro Leu Pro Thr Pro		
25 30 35		
GTC CTG CTG CCT GCT GTG GAC TTT AGC TTG GGA GAA TGG AAA ACC CAG		258
Val Leu Leu Pro Ala Val Asp Phe Ser Leu Gly Glu Trp Lys Thr Gln		
40 45 50		
ATG GAG GAG ACC AAG GCA CAG GAC ATT CTG GGA GCA GTG ACC CTT CTG		306
Met Glu Glu Thr Lys Ala Gln Asp Ile Leu Gly Ala Val Thr Leu Leu		
55 60 65 70		
CTG GAG GGA GTG ATG GCA GCA CGG GGA CAA CTG GGA CCC ACT TGC CTC		354
Leu Glu Gly Val Met Ala Ala Arg Gly Gln Leu Gly Pro Thr Cys Leu		
75 80 85		
TCA TCC CTC CTG GGG CAG CTT TCT GGA CAG GTC CGT CTC CTC CTT GGG		402
Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln Val Arg Leu Leu Gly		
90 95 100		
GCC CTG CAG AGC CTC CTT GGA ACC CAG CTT CCT CCA CAG GGC AGG ACC		450
Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu Pro Pro Gln Gly Arg Thr		
105 110 115		
ACA GCT CAC AAG GAT CCC AAT GCC ATC TTC CTG AGC TTC CAA CAC CTG		498
Thr Ala His Lys Asp Pro Asn Ala Ile Phe Leu Ser Phe Gln His Leu		
120 125 130		
CTC CGA GGA AAG GAC TTC TGG ATT GTT GGA GAC AAA CTT CAC TGC CTC		546
Leu Arg Gly Lys Asp Phe Trp Ile Val Gly Asp Lys Leu His Cys Leu		
135 140 145 150		
AGC CAG AAC TAC TGG CTC TGG GCT TCT GAA GTG GCA GCA GGG ATT CAG		594
Ser Gln Asn Tyr Trp Leu Trp Ala Ser Glu Val Ala Ala Gly Ile Gln		
155 160 165		
AGC CAA GAT TCC TGG TCT GCT GAA CCA AAC CTC CAG GTC CCT GGA CCA		642
Ser Gln Asp Ser Trp Ser Ala Glu Pro Asn Leu Gln Val Pro Gly Pro		
170 175 180		
AAT CCC CGG ATA CCT GAA CAG GAT ACA CGA ACT CTT GAA TGG AAC TCG		690
Asn Pro Arg Ile Pro Glu Gln Asp Thr Arg Thr Leu Glu Trp Asn Ser		
185 190 195		
TGG ACT CTT TCC TGG ACC CTC ACG CAG GAC CCT AGG AGC CCC GGA CAT		738
Trp Thr Leu Ser Trp Thr Leu Thr Gln Asp Pro Arg Ser Pro Gly His		
200 205 210		
TTC CTC AGG AAC ATC AGA CAC AGG CTC CCT GCC ACC CAA CCT CCA GCC		786
Phe Leu Arg Asn Ile Arg His Arg Leu Pro Ala Thr Gln Pro Pro Ala		
215 220 225 230		
TGG ATA TTC TCC TTC CCC AAC CCA TCC TCC TAC TGG ACA GTA TAC GCT		834
Trp Ile Phe Ser Phe Pro Asn Pro Ser Ser Tyr Trp Thr Val Tyr Ala		
235 240 245		

C 13  
cont.

CTT CCC TCT TCC ACC CAC CTT GCC CAC CCC TGT GGT CCA GCT CCA CCC Leu Pro Ser Ser Thr His Leu Ala His Pro Cys Gly Pro Ala Pro Pro	882
250 255 260	
CCT GCT TCC TGACCCCTCT GCTCCAACGC CCACCCCTAC CAGCCCTCTT Pro Ala Ser	931
265	
CTAAACACAT CCTACACCCA CTCCCAGAAT CTGTCTCAGG AAGGGTAAGG TTCTCAGACA	991
CTGCCGACAT CAGCATTGTC TCGTGTACAG CTCCCTTCCC TGCAGGGCGC CCCTGGGAGA	1051
CAACTGGACA AGATTCCTA CTTTCTCCTG AAACCCAAAG CCCTGGTAAA AGGGATACAC	1111
AGGACTGAAA AGGAAATCAT TTTTCACTGT ACATTATAAA CCTTCAGAAG CTA	1164

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 265 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

*cont.*  
Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys Leu Leu  
1 5 10 15  
Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro Glu Val  
20 25 30  
His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe Ser Leu  
35 40 45  
Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp Ile Leu  
50 55 60  
Gly Ala Val Thr Leu Leu Glu Gly Val Met Ala Ala Arg Gly Gln  
65 70 75 80  
Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser Gly Gln  
85 90 95  
Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr Gln Leu  
100 105 110  
Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala Ile Phe  
115 120 125  
Leu Ser Phe Gln His Leu Leu Arg Gly Lys Asp Phe Trp Ile Val Gly  
130 135 140  
Asp Lys Leu His Cys Leu Ser Gln Asn Tyr Trp Leu Trp Ala Ser Glu  
145 150 155 160

Val Ala Ala Gly Ile Gln Ser Gln Asp Ser Trp Ser Ala Glu Pro Asn  
165 170 175

Leu Gln Val Pro Gly Pro Asn Pro Arg Ile Pro Glu Gln Asp Thr Arg  
180 185 190

Thr Leu Glu Trp Asn Ser Trp Thr Leu Ser Trp Thr Leu Thr Gln Asp  
195 200 205

Pro Arg Ser Pro Gly His Phe Leu Arg Asn Ile Arg His Arg Leu Pro  
210 215 220

Ala Thr Gln Pro Pro Ala Trp Ile Phe Ser Phe Pro Asn Pro Ser Ser  
225 230 235 240

Tyr Trp Thr Val Tyr Ala Leu Pro Ser Ser Thr His Leu Ala His Pro  
245 250 255

Cys Gly Pro Ala Pro Pro Ala Ser  
260 265

(2) INFORMATION FOR SEQ ID NO:28:

C13  
wkt.

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 498 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:  
(A) NAME/KEY: CDS  
(B) LOCATION: 1..498

(ix) FEATURE:  
(A) NAME/KEY: mat\_peptide  
(B) LOCATION: 7..498

(ix) FEATURE:  
(A) NAME/KEY: sig\_peptide  
(B) LOCATION: 1..6

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

ATG AAA AGT CCT GCA CCA CCT GCA TGT GAT TTA CGG GTC CTG TCT AAA	48
Met Lys Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys	
-2 1 5 10	
CTG CTG CGC GAC TCT CAC GTG CTG CAC TCT CGT CTG TCC CAG TGC CCG	96
Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro	
15 20 25 30	
GAA GTT CAC CCG CTG CCG ACC CCG GTT CTG CTT CCG GCT GTC GAC TTC	144
Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe	
35 40 45	

TCC CTG GGT GAA TGG AAA ACC CAG ATG GAA GAG ACC AAA GCT CAG GAC Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp 50 55 60	192
ATC CTG GGT GCA GTA ACT CTG CTT CTG GAA GGC GTT ATG GCT GCA CGT Ile Leu Gly Ala Val Thr Leu Leu Glu Gly Val Met Ala Ala Arg 65 70 75	240
GGC CAG CTT GGC CCG ACC TGC CTG TCT TCC CTG CTT GGC CAG CTG TCT Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser 80 85 90	288
GGC CAG GTT CGT CTG CTG CTC GGC GCT CTG CAG TCT CTG CTT GGC ACC Gly Gln Val Arg Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr 95 100 105 110	336
CAG CTG CCG CCA CAG GGC CGT ACC ACT GCT CAC AAG GAT CCG AAC GCT Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala 115 120 125	384
ATC TTC CTG TCT TTC CAG CAC CTG CTG CGT GGC AAA GTT CGT TTC CTG Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu 130 135 140	432
ATG CTG GTT GGC GGT TCT ACC CTG TGC GTT CGT CGG GCG CCG CCA ACC Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr 145 150 155	480
ACT GCT GTT CCG TCT TAA Thr Ala Val Pro Ser *	498
160	

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 166 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Met Lys Ser Pro Ala Pro Pro Ala Cys Asp Leu Arg Val Leu Ser Lys  
-2 1 5 10

Leu Leu Arg Asp Ser His Val Leu His Ser Arg Leu Ser Gln Cys Pro  
15 20 25 30

Glu Val His Pro Leu Pro Thr Pro Val Leu Leu Pro Ala Val Asp Phe  
35 40 45

Ser Leu Gly Glu Trp Lys Thr Gln Met Glu Glu Thr Lys Ala Gln Asp  
50 55 60

*C13  
cont.*

Ile Leu Gly Ala Val Thr Leu Leu Leu Glu Gly Val Met Ala Ala Arg  
65 70 75

Gly Gln Leu Gly Pro Thr Cys Leu Ser Ser Leu Leu Gly Gln Leu Ser  
80 85 90

Gly Gln Val Arg Leu Leu Leu Gly Ala Leu Gln Ser Leu Leu Gly Thr  
95 100 105 110

Gln Leu Pro Pro Gln Gly Arg Thr Thr Ala His Lys Asp Pro Asn Ala  
115 120 125

Ile Phe Leu Ser Phe Gln His Leu Leu Arg Gly Lys Val Arg Phe Leu  
130 135 140

Met Leu Val Gly Gly Ser Thr Leu Cys Val Arg Arg Ala Pro Pro Thr  
145 150 155

Thr Ala Val Pro Ser \*

160

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GAGCTCACTA GTGTCGACCT GCAG

24

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 24 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CTGCAGGTG ACACATAGTGA GCTC

24

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTCATAATTT TTAAAAAATT CATTGACAA ATGCTAAAAT TCTTGATTAA TATTCTCAAT 60  
TGTGAGCGCT CACAATTTAT 80

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

*C<sup>13</sup>*  
*cont.*  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CGATAAATTG TGAGCGCTCA CAATTGAGAA TATTAATCAA GAATTTAGC ATTTGTCAA 60  
TGAATTTTTT AAAAATTATG AGACGT 86

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GACGTCTCAT AATTTTTAAA AAATTCATTT GACAAATGCT AAAATTCTTG ATTAATATTC 60  
TCAATTGTGA GCGCTCACAA TTTATCGAT 89